SEQUENCE LISTING

<110> Tanzi, Rudolph E.
       Kovacs, Dora
       Saunders, Aleister J.

<120> Alpha-2-Macroglobulin Therapies and Drug Screening Methods for
       Alzheimer's Disease

<130> 0609.4460005

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<150> 09/241,606
<151> 1999-02-02

<150> 09/148,503
<151> 1998-09-04

<150> 60/093,297
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Lys Leu Leu His Pro Ser Leu Val Leu Leu Leu Leu Val Leu Leu Pro
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aca gac gcc tca gtc tct gga aaa ccg cag tat atg gtt ctg gtc ccc    151
Thr Asp Ala Ser Val Ser Gly Lys Pro Gln Tyr Met Val Leu Val Pro
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tcc ctg ctc cac act gag acc act gag aag ggc tgt gtc ctt ctg agc    199
Ser Leu Leu His Thr Glu Thr Thr Glu Lys Gly Cys Val Leu Leu Ser
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tac ctg aat gag aca gtg act gta agt gct tcc ttg gag tct gtc agg    247
Tyr Leu Asn Glu Thr Val Thr Val Ser Ala Ser Leu Glu Ser Val Arg
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gga aac agg agc ctc ttc act gac ctg gag gcg gag aat gac gta ctc    295
Gly Asn Arg Ser Leu Phe Thr Asp Leu Glu Ala Glu Asn Asp Val Leu
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cac tgt gtc gcc ttc gct gtc cca aag tct tca tcc aat gag gag gta    343
His Cys Val Ala Phe Ala Val Pro Lys Ser Ser Ser Asn Glu Glu Val
            65                 70                 75
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atg ttc ctc act gtc caa gtg aaa gga cca acc caa gaa ttt aag aag    391
Met Phe Leu Thr Val Gln Val Lys Gly Pro Thr Gln Glu Phe Lys Lys
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cgg acc aca gtg atg gtt aag aac gag gac agt ctg gtc ttt gtc cag    439
Arg Thr Thr Val Met Val Lys Asn Glu Asp Ser Leu Val Phe Val Gln
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aca gac aaa tca atc tac aaa cca ggg cag aca gtg aaa ttt cgt gtt    487
Thr Asp Lys Ser Ile Tyr Lys Pro Gly Gln Thr Val Lys Phe Arg Val
110                115                120                125
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gtc tcc atg gat gaa aac ttt cac ccc ctg aat gag ttg att cca cta   535
Val Ser Met Asp Glu Asn Phe His Pro Leu Asn Glu Leu Ile Pro Leu
            130   135   140

gta tac att cag gat ccc aaa gga aat cgc atc gca caa tgg cag agt   583
Val Tyr Ile Gln Asp Pro Lys Gly Asn Arg Ile Ala Gln Trp Gln Ser
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ttc cag tta gag ggt ggc ctc aag caa ttt tct ttt ccc ctc tca tca   631
Phe Gln Leu Glu Gly Gly Leu Lys Gln Phe Ser Phe Pro Leu Ser Ser
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gag ccc ttc cag ggc tcc tac aag gtg gtg gta cag aag aaa tca ggt   679
Glu Pro Phe Gln Gly Ser Tyr Lys Val Val Val Gln Lys Lys Ser Gly
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gga agg aca gag cac cct ttc acc gtg gag gaa ttt gtt ctt ccc aag   727
Gly Arg Thr Glu His Pro Phe Thr Val Glu Glu Phe Val Leu Pro Lys
190   195   200   205

ttt gaa gta caa gta aca gtg cca aag ata atc acc atc ttg gaa gaa   775
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gag atg aat gta tca gtg tgt ggc cta tac aca tat ggg aag cct gtc   823
Glu Met Asn Val Ser Val Cys Gly Leu Tyr Thr Tyr Gly Lys Pro Val
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cct gga cat gtg act gtg agc att tgc aga aag tat agt gac gct tcc   871
Pro Gly His Val Thr Val Ser Ile Cys Arg Lys Tyr Ser Asp Ala Ser
            240   245   250

gac tgc cac ggt gaa gat tca cag gct ttc tgt gag aaa ttc agt gga   919
Asp Cys His Gly Glu Asp Ser Gln Ala Phe Cys Glu Lys Phe Ser Gly
        255   260   265

cag cta aac agc cat ggc tgc ttc tat cag caa gta aaa acc aag gtc   967
Gln Leu Asn Ser His Gly Cys Phe Tyr Gln Gln Val Lys Thr Lys Val
270   275   280   285

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cag atc caa gaa gaa gga aca gtg gtg gaa ttg act gga agg cag tcc      1063
Gln Ile Gln Glu Glu Gly Thr Val Val Glu Leu Thr Gly Arg Gln Ser
             305                 310                 315


agt gaa atc aca aga acc ata acc aaa ctc tca ttt gtg aaa gtg gac      1111
Ser Glu Ile Thr Arg Thr Ile Thr Lys Leu Ser Phe Val Lys Val Asp
             320                 325                 330


tca cac ttt cga cag gga att ccc ttc ttt ggg cag gtg cgc cta gta      1159
Ser His Phe Arg Gln Gly Ile Pro Phe Phe Gly Gln Val Arg Leu Val
         335                 340                 345


gat ggg aaa ggc gtc cct ata cca aat aaa gtc ata ttc atc aga gga      1207
Asp Gly Lys Gly Val Pro Ile Pro Asn Lys Val Ile Phe Ile Arg Gly
350                 355                 360                 365


aat gaa gca aac tat tac tcc aat gct acc acg gat gag cat ggc ctt      1255
Asn Glu Ala Asn Tyr Tyr Ser Asn Ala Thr Thr Asp Glu His Gly Leu
                 370                 375                 380


gta cag ttc tct atc aac acc acc aac gtt atg ggt acc tct ctt act      1303
Val Gln Phe Ser Ile Asn Thr Thr Asn Val Met Gly Thr Ser Leu Thr
             385                 390                 395


gtt agg gtc aat tac aag gat cgt agt ccc tgt tac ggc tac cag tgg      1351
Val Arg Val Asn Tyr Lys Asp Arg Ser Pro Cys Tyr Gly Tyr Gln Trp
             400                 405                 410


gtg tca gaa gaa cac gaa gag gca cat cac act gct tat ctt gtg ttc      1399
Val Ser Glu Glu His Glu Glu Ala His His Thr Ala Tyr Leu Val Phe
             415                 420                 425


tcc cca agc aag agc ttt gtc cac ctt gag ccc atg tct cat gaa cta      1447
Ser Pro Ser Lys Ser Phe Val His Leu Glu Pro Met Ser His Glu Leu
430                 435                 440                 445


ccc tgt ggc cat act cag aca gtc cag gca cat tat att ctg aat gga      1495
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              Pro Cys Gly His Thr Gln Thr Val Gln Ala His Tyr Ile Leu Asn Gly
                          450                 455                 460


ggc acc ctg ctg ggg ctg aag aag ctc tcc ttt tat tat ctg ata atg      1543
Gly Thr Leu Leu Gly Leu Lys Lys Leu Ser Phe Tyr Tyr Leu Ile Met
            465                 470                 475


gca aag gga ggc att gtc cga act ggg act cat gga ctg ctt gtg aag      1591
Ala Lys Gly Gly Ile Val Arg Thr Gly Thr His Gly Leu Leu Val Lys
            480                 485                 490


cag gaa gac atg aag ggc cat ttt tcc atc tca atc cct gtg aag tca      1639
Gln Glu Asp Met Lys Gly His Phe Ser Ile Ser Ile Pro Val Lys Ser
        495                 500                 505


gac att gct cct gtc gct cgg ttg ctc atc tat gct gtt tta cct acc      1687
Asp Ile Ala Pro Val Ala Arg Leu Leu Ile Tyr Ala Val Leu Pro Thr
510                 515                 520                 525


ggg gac gtg att ggg gat tct gca aaa tat gat gtt gaa aat tgt ctg      1735
Gly Asp Val Ile Gly Asp Ser Ala Lys Tyr Asp Val Glu Asn Cys Leu
                530                 535                 540


gcc aac aag gtg gat ttg agc ttc agc cca tca caa agt ctc cca gcc      1783
Ala Asn Lys Val Asp Leu Ser Phe Ser Pro Ser Gln Ser Leu Pro Ala
            545                 550                 555


tca cac gcc cac ctg cga gtc aca gcg gct cct cag tcc gtc tgc gcc      1831
Ser His Ala His Leu Arg Val Thr Ala Ala Pro Gln Ser Val Cys Ala
            560                 565                 570


ctc cgt gct gtg gac caa agc gtg ctg ctc atg aag cct gat gct gag      1879
Leu Arg Ala Val Asp Gln Ser Val Leu Leu Met Lys Pro Asp Ala Glu
            575                 580                 585


ctc tcg gcg tcc tcg gtt tac aac ctg cta cca gaa aag gac ctc act      1927
Leu Ser Ala Ser Ser Val Tyr Asn Leu Leu Pro Glu Lys Asp Leu Thr
590                 595                 600                 605


ggc ttc cct ggg cct ttg aat gac cag gac gat gaa gac tgc atc aat      1975
Gly Phe Pro Gly Pro Leu Asn Asp Gln Asp Asp Glu Asp Cys Ile Asn
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cgt cat aat gtc tat att aat gga atc aca tat act cca gta tca agt   2023
Arg His Asn Val Tyr Ile Asn Gly Ile Thr Tyr Thr Pro Val Ser Ser
            625                    630                  635


aca aat gaa aag gat atg tac agc ttc cta gag gac atg ggc tta aag   2071
Thr Asn Glu Lys Asp Met Tyr Ser Phe Leu Glu Asp Met Gly Leu Lys
        640                    645                  650


gca ttc acc aac tca aag att cgt aaa ccc aaa atg tgt cca cag ctt   2119
Ala Phe Thr Asn Ser Lys Ile Arg Lys Pro Lys Met Cys Pro Gln Leu
        655                    660                  665


caa cag tat gaa atg cat gga cct gaa ggt cta cgt gta ggt ttt tat   2167
Gln Gln Tyr Glu Met His Gly Pro Glu Gly Leu Arg Val Gly Phe Tyr
670                    675                  680                  685


gag tca gat gta atg gga aga ggc cat gca cgc ctg gtg cat gtt gaa   2215
Glu Ser Asp Val Met Gly Arg Gly His Ala Arg Leu Val His Val Glu
                690                    695                  700


gag cct cac acg gag acc gta cga aag tac ttc cct gag aca tgg atc   2263
Glu Pro His Thr Glu Thr Val Arg Lys Tyr Phe Pro Glu Thr Trp Ile
            705                    710                  715


tgg gat ttg gtg gtg gta aac tca gca ggg gtg gct gag gta gga gta   2311
Trp Asp Leu Val Val Val Asn Ser Ala Gly Val Ala Glu Val Gly Val
        720                    725                  730


aca gtc cct gac acc atc acc gag tgg aag gca ggg gcc ttc tgc ctg   2359
Thr Val Pro Asp Thr Ile Thr Glu Trp Lys Ala Gly Ala Phe Cys Leu
        735                    740                  745


tct gaa gat gct gga ctt ggt atc tct tcc act gcc tct ctc cga gcc   2407
Ser Glu Asp Ala Gly Leu Gly Ile Ser Ser Thr Ala Ser Leu Arg Ala
750                    755                  760                  765


ttc cag ccc ttc ttt gtg gag ctt aca atg cct tac tct gtg att cgt   2455
Phe Gln Pro Phe Phe Val Glu Leu Thr Met Pro Tyr Ser Val Ile Arg
                770                    775                  780
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gga gag gcc ttc aca ctc aag gcc acg gtc cta aac tac ctt ccc aaa   2503
Gly Glu Ala Phe Thr Leu Lys Ala Thr Val Leu Asn Tyr Leu Pro Lys
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tgc atc cgg gtc agt gtg cag ctg gaa gcc tct ccc gcc ttc ctt gct   2551
Cys Ile Arg Val Ser Val Gln Leu Glu Ala Ser Pro Ala Phe Leu Ala
            800                 805                 810

gtc cca gtg gag aag gaa caa gcg cct cac tgc atc tgt gca aac ggg   2599
Val Pro Val Glu Lys Glu Gln Ala Pro His Cys Ile Cys Ala Asn Gly
            815                 820                 825

cgg caa act gtg tcc tgg gca gta acc cca aag tca tta gga aat gtg   2647
Arg Gln Thr Val Ser Trp Ala Val Thr Pro Lys Ser Leu Gly Asn Val
830                 835                 840                 845

aat ttc act gtg agc gca gag gca cta gag tct caa gag ctg tgt ggg   2695
Asn Phe Thr Val Ser Ala Glu Ala Leu Glu Ser Gln Glu Leu Cys Gly
                850                 855                 860

act gag gtg cct tca gtt cct gaa cac gga agg aaa gac aca gtc atc   2743
Thr Glu Val Pro Ser Val Pro Glu His Gly Arg Lys Asp Thr Val Ile
            865                 870                 875

aag cct ctg ttg gtt gaa cct gaa gga cta gag aag gaa aca aca ttc   2791
Lys Pro Leu Leu Val Glu Pro Glu Gly Leu Glu Lys Glu Thr Thr Phe
            880                 885                 890

aac tcc cta ctt tgt cca tca ggt ggt gag gtt tct gaa gaa tta tcc   2839
Asn Ser Leu Leu Cys Pro Ser Gly Gly Glu Val Ser Glu Glu Leu Ser
            895                 900                 905

ctg aaa ctg cca cca aat gtg gta gaa gaa tct gcc cga gct tct gtc   2887
Leu Lys Leu Pro Pro Asn Val Val Glu Glu Ser Ala Arg Ala Ser Val
910                 915                 920                 925

tca gtt ttg gga gac ata tta ggc tct gcc atg caa aac aca caa aat   2935
Ser Val Leu Gly Asp Ile Leu Gly Ser Ala Met Gln Asn Thr Gln Asn
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ctt ctc cag atg ccc tat ggc tgt gga gag cag aat atg gtc ctc ttt   2983
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            945                 950                 955

gct cct aac atc tat gta ctg gat tat cta aat gaa aca cag cag ctt   3031
Ala Pro Asn Ile Tyr Val Leu Asp Tyr Leu Asn Glu Thr Gln Gln Leu
            960                 965                 970

act cca gag atc aag tcc aag gcc att ggc tat ctc aac act ggt tac   3079
Thr Pro Glu Ile Lys Ser Lys Ala Ile Gly Tyr Leu Asn Thr Gly Tyr
            975                 980                 985

cag aga cag ttg aac tac aaa cac tat gat ggc tcc tac agc acc ttt   3127
Gln Arg Gln Leu Asn Tyr Lys His Tyr Asp Gly Ser Tyr Ser Thr Phe
990                 995                 1000                1005

ggg gag cga tat ggc agg aac cag ggc aac acc tgg ctc aca gcc ttt   3175
Gly Glu Arg Tyr Gly Arg Asn Gln Gly Asn Thr Trp Leu Thr Ala Phe
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gtt ctg aag act ttt gcc caa gct cga gcc tac atc ttc atc gat gaa   3223
Val Leu Lys Thr Phe Ala Gln Ala Arg Ala Tyr Ile Phe Ile Asp Glu
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gca cac att acc caa gcc ctc ata tgg ctc tcc cag agg cag aag gac   3271
Ala His Ile Thr Gln Ala Leu Ile Trp Leu Ser Gln Arg Gln Lys Asp
            1040                1045                1050

aat ggc tgt ttc agg agc tct ggg tca ctg ctc aac aat gcc ata aag   3319
Asn Gly Cys Phe Arg Ser Ser Gly Ser Leu Leu Asn Asn Ala Ile Lys
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gga gga gta gaa gat gaa gtg acc ctc tcc gcc tat atc acc atc gcc   3367
Gly Gly Val Glu Asp Glu Val Thr Leu Ser Ala Tyr Ile Thr Ile Ala
1070                1075                1080                1085

ctt ctg gag att cct ctc aca gtc act cac cct gtt gtc cgc aat gcc   3415
Leu Leu Glu Ile Pro Leu Thr Val Thr His Pro Val Val Arg Asn Ala
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ctg ttt tgc ctg gag tca gcc tgg aag aca gca caa gaa ggg gac cat   3463
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               Leu Phe Cys Leu Glu Ser Ala Trp Lys Thr Ala Gln Glu Gly Asp His
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Gly Ser His Val Tyr Thr Lys Ala Leu Leu Ala Tyr Ala Phe Ala Leu
         1120                1125                1130


gca ggt aac cag gac aag agg aag gaa gta ctc aag tca ctt aat gag      3559
Ala Gly Asn Gln Asp Lys Arg Lys Glu Val Leu Lys Ser Leu Asn Glu
         1135                1140                1145


gaa gct gtg aag aaa gac aac tct gtc cat tgg gag cgc cct cag aaa      3607
Glu Ala Val Lys Lys Asp Asn Ser Val His Trp Glu Arg Pro Gln Lys
1150                1155                1160                1165


ccc aag gca cca gtg ggg cat ttt tac gaa ccc cag gct ccc tct gct      3655
Pro Lys Ala Pro Val Gly His Phe Tyr Glu Pro Gln Ala Pro Ser Ala
                  1170                1175                1180


gag gtg gag atg aca tcc tat gtg ctc ctc gct tat ctc acg gcc cag      3703
Glu Val Glu Met Thr Ser Tyr Val Leu Leu Ala Tyr Leu Thr Ala Gln
                  1185                1190                1195


cca gcc cca acc tcg gag gac ctg acc tct gca acc aac atc gtg aag      3751
Pro Ala Pro Thr Ser Glu Asp Leu Thr Ser Ala Thr Asn Ile Val Lys
         1200                1205                1210


tgg atc acg aag cag cag aat gcc cag ggc ggt ttc tcc tcc acc cag      3799
Trp Ile Thr Lys Gln Gln Asn Ala Gln Gly Gly Phe Ser Ser Thr Gln
         1215                1220                1225


gac aca gtg gtg gct ctc cat gct ctg tcc aaa tat gga gcc gcc aca      3847
Asp Thr Val Val Ala Leu His Ala Leu Ser Lys Tyr Gly Ala Ala Thr
1230                1235                1240                1245


ttt acc agg act ggg aag gct gca cag gtg act atc cag tct tca ggg      3895
Phe Thr Arg Thr Gly Lys Ala Ala Gln Val Thr Ile Gln Ser Ser Gly
                  1250                1255                1260


aca ttt tcc agc aaa ttc caa gtg gac aac aac aat cgc ctg tta ctg      3943
Thr Phe Ser Ser Lys Phe Gln Val Asp Asn Asn Asn Arg Leu Leu Leu
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    cag cag gtc tca ttg cca gag ctg cct ggg gaa tac agc atg aaa gtg    3991
    Gln Gln Val Ser Leu Pro Glu Leu Pro Gly Glu Tyr Ser Met Lys Val
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    aca gga gaa gga tgt gtc tac ctc cag acc tcc ttg aaa tac aat att    4039
    Thr Gly Glu Gly Cys Val Tyr Leu Gln Thr Ser Leu Lys Tyr Asn Ile
        1295                      1300                      1305


    ctc cca gaa aag gaa gag ttc ccc ttt gct tta gga gtg cag act ctg    4087
    Leu Pro Glu Lys Glu Glu Phe Pro Phe Ala Leu Gly Val Gln Thr Leu
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    cct caa act tgt gat gaa ccc aaa gcc cac acc agc ttc caa atc tcc    4135
    Pro Gln Thr Cys Asp Glu Pro Lys Ala His Thr Ser Phe Gln Ile Ser
                1330                      1335                      1340


    cta agt gtc agt tac aca ggg agc cgc tct gcc tcc aac atg gcg atc    4183
    Leu Ser Val Ser Tyr Thr Gly Ser Arg Ser Ala Ser Asn Met Ala Ile
                1345                      1350                      1355


    gtt gat gtg aag atg gtc tct ggc ttc att ccc ctg aag cca aca gtg    4231
    Val Asp Val Lys Met Val Ser Gly Phe Ile Pro Leu Lys Pro Thr Val
            1360                      1365                      1370


    aaa atg ctt gaa aga tct aac cat gtg agc cgg aca gaa gtc agc agc    4279
    Lys Met Leu Glu Arg Ser Asn His Val Ser Arg Thr Glu Val Ser Ser
        1375                      1380                      1385


    aac cat gtc ttg att tac ctt gat aag gtg tca aat cag aca ctg agc    4327
    Asn His Val Leu Ile Tyr Leu Asp Lys Val Ser Asn Gln Thr Leu Ser
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    ttg ttc ttc acg gtt ctg caa gat gtc cca gta aga gat ctc aaa cca    4375
    Leu Phe Phe Thr Val Leu Gln Asp Val Pro Val Arg Asp Leu Lys Pro
                1410                      1415                      1420


    gcc ata gtg aaa gtc tat gat tac tac gag acg gat gag ttt gca atc    4423
    Ala Ile Val Lys Val Tyr Asp Tyr Tyr Glu Thr Asp Glu Phe Ala Ile
                1425                      1430                      1435
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Ala Glu Tyr Asn Ala Pro Cys Ser Lys Asp Leu Gly Asn Ala
        1440            1445            1450


agaccacaag gctgaaaagt gctttgctgg agtcctgttc tctgagctcc acagaagaca 4528

cgtgtttttg tatctttaaa gacttgatga ataaacactt tttctggtc               4577
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Val Leu Val Pro Ser Leu Leu His Thr Glu Thr Thr Glu Lys Gly Cys
            35                40                45


Val Leu Leu Ser Tyr Leu Asn Glu Thr Val Thr Val Ser Ala Ser Leu
        50                55                60


Glu Ser Val Arg Gly Asn Arg Ser Leu Phe Thr Asp Leu Glu Ala Glu
 65                70                75                80


Asn Asp Val Leu His Cys Val Ala Phe Ala Val Pro Lys Ser Ser Ser
                85                90                95


Asn Glu Glu Val Met Phe Leu Thr Val Gln Val Lys Gly Pro Thr Gln
            100               105               110


Glu Phe Lys Lys Arg Thr Thr Val Met Val Lys Asn Glu Asp Ser Leu
        115               120               125


Val Phe Val Gln Thr Asp Lys Ser Ile Tyr Lys Pro Gly Gln Thr Val
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              130                   135                   140

Lys Phe Arg Val Val Ser Met Asp Glu Asn Phe His Pro Leu Asn Glu
145                 150                 155                 160

Leu Ile Pro Leu Val Tyr Ile Gln Asp Pro Lys Gly Asn Arg Ile Ala
                165                 170                 175

Gln Trp Gln Ser Phe Gln Leu Glu Gly Gly Leu Lys Gln Phe Ser Phe
                180                 185                 190

Pro Leu Ser Ser Glu Pro Phe Gln Gly Ser Tyr Lys Val Val Val Gln
            195                 200                 205

Lys Lys Ser Gly Gly Arg Thr Glu His Pro Phe Thr Val Glu Glu Phe
    210                 215                 220

Val Leu Pro Lys Phe Glu Val Gln Val Thr Val Pro Lys Ile Ile Thr
225                 230                 235                 240

Ile Leu Glu Glu Glu Met Asn Val Ser Val Cys Gly Leu Tyr Thr Tyr
                245                 250                 255

Gly Lys Pro Val Pro Gly His Val Thr Val Ser Ile Cys Arg Lys Tyr
                260                 265                 270

Ser Asp Ala Ser Asp Cys His Gly Glu Asp Ser Gln Ala Phe Cys Glu
            275                 280                 285

Lys Phe Ser Gly Gln Leu Asn Ser His Gly Cys Phe Tyr Gln Gln Val
            290                 295                 300

Lys Thr Lys Val Phe Gln Leu Lys Arg Lys Glu Tyr Glu Met Lys Leu
305                 310                 315                 320

His Thr Glu Ala Gln Ile Gln Glu Glu Gly Thr Val Val Glu Leu Thr
                325                 330                 335

Gly Arg Gln Ser Ser Glu Ile Thr Arg Thr Ile Thr Lys Leu Ser Phe
            340                 345                 350
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Val Lys Val Asp Ser His Phe Arg Gln Gly Ile Pro Phe Phe Gly Gln
        355                 360                 365

Val Arg Leu Val Asp Gly Lys Gly Val Pro Ile Pro Asn Lys Val Ile
        370                 375                 380

Phe Ile Arg Gly Asn Glu Ala Asn Tyr Tyr Ser Asn Ala Thr Thr Asp
385                 390                 395                 400

Glu His Gly Leu Val Gln Phe Ser Ile Asn Thr Thr Asn Val Met Gly
                405                 410                 415

Thr Ser Leu Thr Val Arg Val Asn Tyr Lys Asp Arg Ser Pro Cys Tyr
                420                 425                 430

Gly Tyr Gln Trp Val Ser Glu Glu His Glu Glu Ala His His Thr Ala
        435                 440                 445

Tyr Leu Val Phe Ser Pro Ser Lys Ser Phe Val His Leu Glu Pro Met
        450                 455                 460

Ser His Glu Leu Pro Cys Gly His Thr Gln Thr Val Gln Ala His Tyr
465                 470                 475                 480

Ile Leu Asn Gly Gly Thr Leu Leu Gly Leu Lys Lys Leu Ser Phe Tyr
                485                 490                 495

Tyr Leu Ile Met Ala Lys Gly Gly Ile Val Arg Thr Gly Thr His Gly
                500                 505                 510

Leu Leu Val Lys Gln Glu Asp Met Lys Gly His Phe Ser Ile Ser Ile
                515                 520                 525

Pro Val Lys Ser Asp Ile Ala Pro Val Ala Arg Leu Leu Ile Tyr Ala
        530                 535                 540

Val Leu Pro Thr Gly Asp Val Ile Gly Asp Ser Ala Lys Tyr Asp Val
545                 550                 555                 560

Glu Asn Cys Leu Ala Asn Lys Val Asp Leu Ser Phe Ser Pro Ser Gln
                565                 570                 575
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Ser Leu Pro Ala Ser His Ala His Leu Arg Val Thr Ala Ala Pro Gln
        580   585   590

Ser Val Cys Ala Leu Arg Ala Val Asp Gln Ser Val Leu Leu Met Lys
        595   600   605

Pro Asp Ala Glu Leu Ser Ala Ser Ser Val Tyr Asn Leu Leu Pro Glu
        610   615   620

Lys Asp Leu Thr Gly Phe Pro Gly Pro Leu Asn Asp Gln Asp Asp Glu
625   630   635   640

Asp Cys Ile Asn Arg His Asn Val Tyr Ile Asn Gly Ile Thr Tyr Thr
                645   650   655

Pro Val Ser Ser Thr Asn Glu Lys Asp Met Tyr Ser Phe Leu Glu Asp
        660   665   670

Met Gly Leu Lys Ala Phe Thr Asn Ser Lys Ile Arg Lys Pro Lys Met
        675   680   685

Cys Pro Gln Leu Gln Gln Tyr Glu Met His Gly Pro Glu Gly Leu Arg
        690   695   700

Val Gly Phe Tyr Glu Ser Asp Val Met Gly Arg Gly His Ala Arg Leu
705   710   715   720

Val His Val Glu Glu Pro His Thr Glu Thr Val Arg Lys Tyr Phe Pro
                725   730   735

Glu Thr Trp Ile Trp Asp Leu Val Val Val Asn Ser Ala Gly Val Ala
        740   745   750

Glu Val Gly Val Thr Val Pro Asp Thr Ile Thr Glu Trp Lys Ala Gly
        755   760   765

Ala Phe Cys Leu Ser Glu Asp Ala Gly Leu Gly Ile Ser Ser Thr Ala
        770   775   780

Ser Leu Arg Ala Phe Gln Pro Phe Phe Val Glu Leu Thr Met Pro Tyr

785   790   795   800

Ser Val Ile Arg Gly Glu Ala Phe Thr Leu Lys Ala Thr Val Leu Asn
                805   810   815

Tyr Leu Pro Lys Cys Ile Arg Val Ser Val Gln Leu Glu Ala Ser Pro
                820   825   830

Ala Phe Leu Ala Val Pro Val Glu Lys Glu Gln Ala Pro His Cys Ile
                835   840   845

Cys Ala Asn Gly Arg Gln Thr Val Ser Trp Ala Val Thr Pro Lys Ser
                850   855   860

Leu Gly Asn Val Asn Phe Thr Val Ser Ala Glu Ala Leu Glu Ser Gln
865   870   875   880

Glu Leu Cys Gly Thr Glu Val Pro Ser Val Pro Glu His Gly Arg Lys
                885   890   895

Asp Thr Val Ile Lys Pro Leu Leu Val Glu Pro Glu Gly Leu Glu Lys
                900   905   910

Glu Thr Thr Phe Asn Ser Leu Leu Cys Pro Ser Gly Gly Glu Val Ser
                915   920   925

Glu Glu Leu Ser Leu Lys Leu Pro Pro Asn Val Val Glu Glu Ser Ala
                930   935   940

Arg Ala Ser Val Ser Val Leu Gly Asp Ile Leu Gly Ser Ala Met Gln
945   950   955   960

Asn Thr Gln Asn Leu Leu Gln Met Pro Tyr Gly Cys Gly Glu Gln Asn
                965   970   975

Met Val Leu Phe Ala Pro Asn Ile Tyr Val Leu Asp Tyr Leu Asn Glu
                980   985   990

Thr Gln Gln Leu Thr Pro Glu Ile Lys Ser Lys Ala Ile Gly Tyr Leu
                995   1000   1005

Asn Thr Gly Tyr Gln Arg Gln Leu Asn Tyr Lys His Tyr Asp Gly Ser
    1010   1015   1020

Tyr Ser Thr Phe Gly Glu Arg Tyr Gly Arg Asn Gln Gly Asn Thr Trp
1025   1030   1035   1040

Leu Thr Ala Phe Val Leu Lys Thr Phe Ala Gln Ala Arg Ala Tyr Ile
         1045   1050   1055

Phe Ile Asp Glu Ala His Ile Thr Gln Ala Leu Ile Trp Leu Ser Gln
        1060   1065   1070

Arg Gln Lys Asp Asn Gly Cys Phe Arg Ser Ser Gly Ser Leu Leu Asn
      1075   1080   1085

Asn Ala Ile Lys Gly Gly Val Glu Asp Glu Val Thr Leu Ser Ala Tyr
    1090   1095   1100

Ile Thr Ile Ala Leu Leu Glu Ile Pro Leu Thr Val Thr His Pro Val
1105   1110   1115   1120

Val Arg Asn Ala Leu Phe Cys Leu Glu Ser Ala Trp Lys Thr Ala Gln
        1125   1130   1135

Glu Gly Asp His Gly Ser His Val Tyr Thr Lys Ala Leu Leu Ala Tyr
        1140   1145   1150

Ala Phe Ala Leu Ala Gly Asn Gln Asp Lys Arg Lys Glu Val Leu Lys
        1155   1160   1165

Ser Leu Asn Glu Glu Ala Val Lys Lys Asp Asn Ser Val His Trp Glu
    1170   1175   1180

Arg Pro Gln Lys Pro Lys Ala Pro Val Gly His Phe Tyr Glu Pro Gln
1185   1190   1195   1200

Ala Pro Ser Ala Glu Val Glu Met Thr Ser Tyr Val Leu Leu Ala Tyr
        1205   1210   1215

Leu Thr Ala Gln Pro Ala Pro Thr Ser Glu Asp Leu Thr Ser Ala Thr
        1220   1225   1230

Asn Ile Val Lys Trp Ile Thr Lys Gln Gln Asn Ala Gln Gly Gly Phe
        1235   1240   1245

Ser Ser Thr Gln Asp Thr Val Val Ala Leu His Ala Leu Ser Lys Tyr
        1250   1255   1260

Gly Ala Ala Thr Phe Thr Arg Thr Gly Lys Ala Ala Gln Val Thr Ile
1265   1270   1275   1280

Gln Ser Ser Gly Thr Phe Ser Ser Lys Phe Gln Val Asp Asn Asn Asn
                1285   1290   1295

Arg Leu Leu Leu Gln Gln Val Ser Leu Pro Glu Leu Pro Gly Glu Tyr
                1300   1305   1310

Ser Met Lys Val Thr Gly Glu Gly Cys Val Tyr Leu Gln Thr Ser Leu
        1315   1320   1325

Lys Tyr Asn Ile Leu Pro Glu Lys Glu Glu Phe Pro Phe Ala Leu Gly
        1330   1335   1340

Val Gln Thr Leu Pro Gln Thr Cys Asp Glu Pro Lys Ala His Thr Ser
1345   1350   1355   1360

Phe Gln Ile Ser Leu Ser Val Ser Tyr Thr Gly Ser Arg Ser Ala Ser
                1365   1370   1375

Asn Met Ala Ile Val Asp Val Lys Met Val Ser Gly Phe Ile Pro Leu
                1380   1385   1390

Lys Pro Thr Val Lys Met Leu Glu Arg Ser Asn His Val Ser Arg Thr
        1395   1400   1405

Glu Val Ser Ser Asn His Val Leu Ile Tyr Leu Asp Lys Val Ser Asn
        1410   1415   1420

Gln Thr Leu Ser Leu Phe Phe Thr Val Leu Gln Asp Val Pro Val Arg
1425   1430   1435   1440

Asp Leu Lys Pro Ala Ile Val Lys Val Tyr Asp Tyr Tyr Glu Thr Asp

```
                1445                    1450                    1455


Glu Phe Ala Ile Ala Glu Tyr Asn Ala Pro Cys Ser Lys Asp Leu Gly
            1460                    1465                    1470


Asn Ala



<210> 3
<211> 750
<212> DNA
<213> Homo sapiens


<220>
<221> CDS
<222> (1)..(750)
<223> Aβ/LRP Binding Domain


<400> 3
tcg gag gac ctg acc tct gca acc aac atc gtg aag tgg atc acg aag        48
Ser Glu Asp Leu Thr Ser Ala Thr Asn Ile Val Lys Trp Ile Thr Lys
  1               5                  10                  15


cag cag aat gcc cag ggc ggt ttc tcc tcc acc cag gac aca gtg gtg        96
Gln Gln Asn Ala Gln Gly Gly Phe Ser Ser Thr Gln Asp Thr Val Val
                20                  25                  30


gct ctc cat gct ctg tcc aaa tat gga gcc gcc aca ttt acc agg act       144
Ala Leu His Ala Leu Ser Lys Tyr Gly Ala Ala Thr Phe Thr Arg Thr
            35                  40                  45


ggg aag gct gca cag gtg act atc cag tct tca ggg aca ttt tcc agc       192
Gly Lys Ala Ala Gln Val Thr Ile Gln Ser Ser Gly Thr Phe Ser Ser
        50                  55                  60


aaa ttc caa gtg gac aac aac aat cgc ctg tta ctg cag cag gtc tca       240
Lys Phe Gln Val Asp Asn Asn Asn Arg Leu Leu Leu Gln Gln Val Ser
 65                  70                  75                  80


ttg cca gag ctg cct ggg gaa tac agc atg aaa gtg aca gga gaa gga       288
Leu Pro Glu Leu Pro Gly Glu Tyr Ser Met Lys Val Thr Gly Glu Gly
```

```
                    85                      90                      95

tgt gtc tac ctc cag acc tcc ttg aaa tac aat att ctc cca gaa aag    336
Cys Val Tyr Leu Gln Thr Ser Leu Lys Tyr Asn Ile Leu Pro Glu Lys
            100                 105                 110


gaa gag ttc ccc ttt gct tta gga gtg cag act ctg cct caa act tgt    384
Glu Glu Phe Pro Phe Ala Leu Gly Val Gln Thr Leu Pro Gln Thr Cys
            115                 120                 125


gat gaa ccc aaa gcc cac acc agc ttc caa atc tcc cta agt gtc agt    432
Asp Glu Pro Lys Ala His Thr Ser Phe Gln Ile Ser Leu Ser Val Ser
            130                 135                 140


tac aca ggg agc cgc tct gcc tcc aac atg gcg atc gtt gat gtg aag    480
Tyr Thr Gly Ser Arg Ser Ala Ser Asn Met Ala Ile Val Asp Val Lys
145                 150                 155                 160


atg gtc tct ggc ttc att ccc ctg aag cca aca gtg aaa atg ctt gaa    528
Met Val Ser Gly Phe Ile Pro Leu Lys Pro Thr Val Lys Met Leu Glu
                165                 170                 175


aga tct aac cat gtg agc cgg aca gaa gtc agc agc aac cat gtc ttg    576
Arg Ser Asn His Val Ser Arg Thr Glu Val Ser Ser Asn His Val Leu
            180                 185                 190


att tac ctt gat aag gtg tca aat cag aca ctg agc ttg ttc ttc acg    624
Ile Tyr Leu Asp Lys Val Ser Asn Gln Thr Leu Ser Leu Phe Phe Thr
            195                 200                 205


gtt ctg caa gat gtc cca gta aga gat ctc aaa cca gcc ata gtg aaa    672
Val Leu Gln Asp Val Pro Val Arg Asp Leu Lys Pro Ala Ile Val Lys
            210                 215                 220


gtc tat gat tac tac gag acg gat gag ttt gca atc gct gag tac aat    720
Val Tyr Asp Tyr Tyr Glu Thr Asp Glu Phe Ala Ile Ala Glu Tyr Asn
225                 230                 235                 240


gct cct tgc agc aaa gat ctt gga aat gct                            750
Ala Pro Cys Ser Lys Asp Leu Gly Asn Ala
                245                 250
```

<210> 4
<211> 250
<212> PRT
<213> Homo sapiens

<400> 4
Ser Glu Asp Leu Thr Ser Ala Thr Asn Ile Val Lys Trp Ile Thr Lys
 1   5   10   15

Gln Gln Asn Ala Gln Gly Gly Phe Ser Ser Thr Gln Asp Thr Val Val
            20   25   30

Ala Leu His Ala Leu Ser Lys Tyr Gly Ala Ala Thr Phe Thr Arg Thr
        35   40   45

Gly Lys Ala Ala Gln Val Thr Ile Gln Ser Ser Gly Thr Phe Ser Ser
    50   55   60

Lys Phe Gln Val Asp Asn Asn Asn Arg Leu Leu Leu Gln Gln Val Ser
65   70   75   80

Leu Pro Glu Leu Pro Gly Glu Tyr Ser Met Lys Val Thr Gly Glu Gly
                85   90   95

Cys Val Tyr Leu Gln Thr Ser Leu Lys Tyr Asn Ile Leu Pro Glu Lys
            100   105   110

Glu Glu Phe Pro Phe Ala Leu Gly Val Gln Thr Leu Pro Gln Thr Cys
        115   120   125

Asp Glu Pro Lys Ala His Thr Ser Phe Gln Ile Ser Leu Ser Val Ser
        130   135   140

Tyr Thr Gly Ser Arg Ser Ala Ser Asn Met Ala Ile Val Asp Val Lys
145   150   155   160

Met Val Ser Gly Phe Ile Pro Leu Lys Pro Thr Val Lys Met Leu Glu
                165   170   175

```
Arg Ser Asn His Val Ser Arg Thr Glu Val Ser Ser Asn His Val Leu
            180               185                   190

Ile Tyr Leu Asp Lys Val Ser Asn Gln Thr Leu Ser Leu Phe Phe Thr
            195               200                   205

Val Leu Gln Asp Val Pro Val Arg Asp Leu Lys Pro Ala Ile Val Lys
            210               215               220

Val Tyr Asp Tyr Tyr Glu Thr Asp Glu Phe Ala Ile Ala Glu Tyr Asn
225               230               235                   240

Ala Pro Cys Ser Lys Asp Leu Gly Asn Ala
                    245               250
```

```
<210> 5
<211> 333
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(333)
<223> Aβ Binding Domain

<400> 5
tcg gag gac ctg acc tct gca acc aac atc gtg aag tgg atc acg aag      48
Ser Glu Asp Leu Thr Ser Ala Thr Asn Ile Val Lys Trp Ile Thr Lys
 1               5                   10                  15

cag cag aat gcc cag ggc ggt ttc tcc tcc acc cag gac aca gtg gtg      96
Gln Gln Asn Ala Gln Gly Gly Phe Ser Ser Thr Gln Asp Thr Val Val
                20                  25                  30

gct ctc cat gct ctg tcc aaa tat gga gcc gcc aca ttt acc agg act     144
Ala Leu His Ala Leu Ser Lys Tyr Gly Ala Ala Thr Phe Thr Arg Thr
            35                  40                  45

ggg aag gct gca cag gtg act atc cag tct tca ggg aca ttt tcc agc     192
Gly Lys Ala Ala Gln Val Thr Ile Gln Ser Ser Gly Thr Phe Ser Ser
```

```
        50                      55                      60

aaa ttc caa gtg gac aac aac aat cgc ctg tta ctg cag cag gtc tca   240
Lys Phe Gln Val Asp Asn Asn Asn Arg Leu Leu Leu Gln Gln Val Ser
 65                  70                  75                  80


ttg cca gag ctg cct ggg gaa tac agc atg aaa gtg aca gga gaa gga   288
Leu Pro Glu Leu Pro Gly Glu Tyr Ser Met Lys Val Thr Gly Glu Gly
                    85                  90                  95


tgt gtc tac ctc cag acc tcc ttg aaa tac aat att ctc cca gaa       333
Cys Val Tyr Leu Gln Thr Ser Leu Lys Tyr Asn Ile Leu Pro Glu
                100                 105                 110
```

<210> 6
<211> 111
<212> PRT
<213> Homo sapiens

<400> 6

```
Ser Glu Asp Leu Thr Ser Ala Thr Asn Ile Val Lys Trp Ile Thr Lys
 1               5                   10                  15


Gln Gln Asn Ala Gln Gly Gly Phe Ser Ser Thr Gln Asp Thr Val Val
                20                  25                  30


Ala Leu His Ala Leu Ser Lys Tyr Gly Ala Ala Thr Phe Thr Arg Thr
            35                  40                  45


Gly Lys Ala Ala Gln Val Thr Ile Gln Ser Ser Gly Thr Phe Ser Ser
        50                  55                  60


Lys Phe Gln Val Asp Asn Asn Asn Arg Leu Leu Leu Gln Gln Val Ser
 65                  70                  75                  80


Leu Pro Glu Leu Pro Gly Glu Tyr Ser Met Lys Val Thr Gly Glu Gly
                85                  90                  95


Cys Val Tyr Leu Gln Thr Ser Leu Lys Tyr Asn Ile Leu Pro Glu
                100                 105                 110
```

<210> 7
<211> 417
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(417)
<223> LRP Binding Domain

<400> 7

```
aag gaa gag ttc ccc ttt gct tta gga gtg cag act ctg cct caa act    48
Lys Glu Glu Phe Pro Phe Ala Leu Gly Val Gln Thr Leu Pro Gln Thr
  1               5                  10                  15


tgt gat gaa ccc aaa gcc cac acc agc ttc caa atc tcc cta agt gtc    96
Cys Asp Glu Pro Lys Ala His Thr Ser Phe Gln Ile Ser Leu Ser Val
             20                  25                  30


agt tac aca ggg agc cgc tct gcc tcc aac atg gcg atc gtt gat gtg   144
Ser Tyr Thr Gly Ser Arg Ser Ala Ser Asn Met Ala Ile Val Asp Val
          35                  40                  45


aag atg gtc tct ggc ttc att ccc ctg aag cca aca gtg aaa atg ctt   192
Lys Met Val Ser Gly Phe Ile Pro Leu Lys Pro Thr Val Lys Met Leu
       50                  55                  60


gaa aga tct aac cat gtg agc cgg aca gaa gtc agc agc aac cat gtc   240
Glu Arg Ser Asn His Val Ser Arg Thr Glu Val Ser Ser Asn His Val
 65                  70                  75                  80


ttg att tac ctt gat aag gtg tca aat cag aca ctg agc ttg ttc ttc   288
Leu Ile Tyr Leu Asp Lys Val Ser Asn Gln Thr Leu Ser Leu Phe Phe
                85                  90                  95


acg gtt ctg caa gat gtc cca gta aga gat ctc aaa cca gcc ata gtg   336
Thr Val Leu Gln Asp Val Pro Val Arg Asp Leu Lys Pro Ala Ile Val
            100                 105                 110
```

```
aaa gtc tat gat tac tac gag acg gat gag ttt gca atc gct gag tac     384
Lys Val Tyr Asp Tyr Tyr Glu Thr Asp Glu Phe Ala Ile Ala Glu Tyr
        115                 120                 125


aat gct cct tgc agc aaa gat ctt gga aat gct                         417
Asn Ala Pro Cys Ser Lys Asp Leu Gly Asn Ala
        130                 135
```

<210> 8
<211> 139
<212> PRT
<213> Homo sapiens

<400> 8

```
Lys Glu Glu Phe Pro Phe Ala Leu Gly Val Gln Thr Leu Pro Gln Thr
 1               5                   10                  15


Cys Asp Glu Pro Lys Ala His Thr Ser Phe Gln Ile Ser Leu Ser Val
                20                  25                  30


Ser Tyr Thr Gly Ser Arg Ser Ala Ser Asn Met Ala Ile Val Asp Val
            35                  40                  45


Lys Met Val Ser Gly Phe Ile Pro Leu Lys Pro Thr Val Lys Met Leu
    50                  55                  60


Glu Arg Ser Asn His Val Ser Arg Thr Glu Val Ser Ser Asn His Val
65                  70                  75                  80


Leu Ile Tyr Leu Asp Lys Val Ser Asn Gln Thr Leu Ser Leu Phe Phe
                85                  90                  95


Thr Val Leu Gln Asp Val Pro Val Arg Asp Leu Lys Pro Ala Ile Val
            100                 105                 110


Lys Val Tyr Asp Tyr Tyr Glu Thr Asp Glu Phe Ala Ile Ala Glu Tyr
        115                 120                 125


Asn Ala Pro Cys Ser Lys Asp Leu Gly Asn Ala
        130                 135
```

<210> 9
<211> 81
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(81)
<223> Consensus LRP Binding Domain

<400> 9
ttc att ccc ctg aag cca aca gtg aaa atg ctt gaa aga tct aac cat   48
Phe Ile Pro Leu Lys Pro Thr Val Lys Met Leu Glu Arg Ser Asn His
  1   5   10   15

gtg agc cgg aca gaa gtc agc agc aac cat gtc   81
Val Ser Arg Thr Glu Val Ser Ser Asn His Val
            20   25

<210> 10
<211> 27
<212> PRT
<213> Homo sapiens

<400> 10
Phe Ile Pro Leu Lys Pro Thr Val Lys Met Leu Glu Arg Ser Asn His
  1   5   10   15

Val Ser Arg Thr Glu Val Ser Ser Asn His Val
            20   25

<210> 11
<211> 33
<212> DNA
<213> Homo sapiens

<220>

<221> CDS
<222> (1)..(33)
<223> Aβ Fibril Inhibitor

<400> 11
cgc gat ctg cca ttc ttc cca gtc cca att gat   33
Arg Asp Leu Pro Phe Phe Pro Val Pro Ile Asp
 1   5   10

<210> 12
<211> 11
<212> PRT
<213> Homo sapiens

<400> 12
Arg Asp Leu Pro Phe Phe Pro Val Pro Ile Asp
 1   5   10

<210> 13
<211> 114
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(114)
<223> Aβ Fibril Inhibitor

<400> 13
cgc gat ctg cca ttc ttc cca gtc cca att gat ttc att ccc ctg aag   48
Arg Asp Leu Pro Phe Phe Pro Val Pro Ile Asp Phe Ile Pro Leu Lys
 1   5   10   15

cca aca gtg aaa atg ctt gaa aga tct aac cat gtg agc cgg aca gaa   96
Pro Thr Val Lys Met Leu Glu Arg Ser Asn His Val Ser Arg Thr Glu
            20   25   30

gtc agc agc aac cat gtc   114
Val Ser Ser Asn His Val

35

<210> 14
<211> 38
<212> PRT
<213> Homo sapiens

<400> 14
Arg Asp Leu Pro Phe Phe Pro Val Pro Ile Asp Phe Ile Pro Leu Lys
 1   5   10   15

Pro Thr Val Lys Met Leu Glu Arg Ser Asn His Val Ser Arg Thr Glu
                20   25   30

Val Ser Ser Asn His Val
            35

<210> 15
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(27)

<400> 15
cgc gat ctg cca ttc ttc cca gtc gat   27
Arg Asp Leu Pro Phe Phe Pro Val Asp
 1   5

<210> 16
<211> 9
<212> PRT
<213> Homo sapiens

<400> 16
Arg Asp Leu Pro Phe Phe Pro Val Asp

1   5

<210> 17
<211> 21
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(21)

<400> 17
ctg cca ttc ttc cca gtc gat   21
Leu Pro Phe Phe Pro Val Asp
  1   5

<210> 18
<211> 7
<212> PRT
<213> Homo sapiens

<400> 18
Leu Pro Phe Phe Pro Val Asp
  1   5

<210> 19
<211> 18
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(18)

<400> 19
ctg cca ttc ttc gtc gat   18
Leu Pro Phe Phe Val Asp
  1   5

```
<210> 20
<211> 6
<212> PRT
<213> Homo sapiens

<400> 20
Leu Pro Phe Phe Val Asp
 1               5
```

```
<210> 21
<211> 15
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(15)

<400> 21
ctg cca ttc ttc gat                                              15
Leu Pro Phe Phe Asp
 1               5
```

```
<210> 22
<211> 5
<212> PRT
<213> Homo sapiens

<400> 22
Leu Pro Phe Phe Asp
 1               5
```

```
<210> 23
<211> 12
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> (1)..(12)

<400> 23
ctg cca ttc ttc                                                    12
Leu Pro Phe Phe
  1


<210> 24
<211> 4
<212> PRT
<213> Homo sapiens

<400> 24
Leu Pro Phe Phe
  1


<210> 25
<211> 9
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(9)

<400> 25
cca ttc ttc                                                         9
Pro Phe Phe
  1


<210> 26
<211> 3
<212> PRT
<213> Homo sapiens
```

<400> 26

Pro Phe Phe
  1

<210> 27

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<223> Noncoding-antisense DNA

<400> 27

catgcaccag gcgtgcatgg cctcttccca ttacatctga ctctgagtga   50